

Serial Number: 09/684,215A

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☒ Inserted mandatory headings, specifically: C2207 globally
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/09/684,215A

TIME: 09:31:03

Input Set : A:\-80-1.app

Output Set: N:\CRF3\04162002\I684215A.raw

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255 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
256          85          90          95
258 gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg 336
259 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
260          100          105          110
262 caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag 384
263 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
264          115          120          125
266 gga ccc ccg gcc 396
267 Gly Pro Pro Ala
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272 <211> LENGTH: 132
273 <212> TYPE: PRT
274 <213> ORGANISM: Mycobacterium tuberculosis ><220>
275 <223> OTHER INFORMATION: 14 KD C-terminal fragment of MTB32A Ral2
277 <400> SEQUENCE: 4
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280 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
281 20 25 30
282 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
283 35 40 45
284 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
285 50 55 60
286 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
287 65 70 75 80
288 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
289 85 90 95
290 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
291 100 105 110
292 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
293 115 120 125
294 Gly Pro Pro Ala
295 130
298 <210> SEQ ID NO: 5
299 <211> LENGTH: 702
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <221> NAME/KEY: CDS
305 <222> LOCATION: (4)..(696)
306 <223> OTHER INFORMATION: Ral2-DPPD fusion polypeptide
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence:Ral2-DPPD fusion
310 , polypeptide
312 <400> SEQUENCE: 5

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1600

RAW SEQUENCE LISTING DATE: 04/16/2002
 PATENT APPLICATION: US/09/684,215A TIME: 11:24:16

Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF3\04162002\I684215A.raw

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3 <110> APPLICANT: Skeiky, Yasir
4     Guderian, Jeffrey
5     Corixa Corporation
7 <120> TITLE OF INVENTION: Methods of Using a Mycobacterium tuberculosis Coding
8     Sequence to Facilitate Stable and High Yield Expression
9     of Heterologous Proteins
11 <130> FILE REFERENCE: 014058-008010US
13 <140> CURRENT APPLICATION NUMBER: US 09/684,215A
14 <141> CURRENT FILING DATE: 2000-10-06
16 <150> PRIOR APPLICATION NUMBER: US 60/158,585
17 <151> PRIOR FILING DATE: 1999-10-07
19 <160> NUMBER OF SEQ ID NOS: 22
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1872
25 <212> TYPE: DNA
26 <213> ORGANISM: Mycobacterium tuberculosis
28 <220> FEATURE:
29 <223> OTHER INFORMATION: 32 KD serine protease MTB32A
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (89)..(1156)
34 <223> OTHER INFORMATION: MTB32A
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37 <221> NAME/KEY: sig_peptide
38 <222> LOCATION: (89)..(184)
39 <223> OTHER INFORMATION: N-terminal hydrophobic secretory signal sequence
41 <220> FEATURE:
42 <221> NAME/KEY: mat_peptide
43 <222> LOCATION: (185)..(1153)
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48 tagctacccc gacacaggag gttacggg atg agc aat tcg cgc cgc cgc tca 112
49                               Met Ser Asn Ser Arg Arg Arg Ser
50                               -30                               -25
52 ctc agg tgg tca tgg ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc 160
53 Leu Arg Trp Ser Trp Leu Leu Ser Val Leu Ala Ala Val Gly Leu Gly
54                               -20                               -15                               -10
56 ctg gcc acg gcg ccg gcc cag gcg gcc ccg ccg gcc ttg tcg cag gac 208
57 Leu Ala Thr Ala Pro Ala Gln Ala Ala Pro Pro Ala Leu Ser Gln Asp
58                               -5                               -1    1                               5
60 cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc 256
61 Arg Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val

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DATE: 04/16/2002

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Output Set: N:\CRF3\04162002\I684215A.raw

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65	Ala	Gln	Val	Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr	
66	25	30	35	40	
68	aac	aac	gcc	gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt	352
69	Asn	Asn	Ala	Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly	
70		45	50	55	
72	gtc	gtg	ctg	acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat	400
73	Val	Val	Leu	Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn	
74		60	65	70	
76	gcg	ttc	agc	gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg	448
77	Ala	Phe	Ser	Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly	
78		75	80	85	
80	tat	gac	cgc	acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt	496
81	Tyr	Asp	Arg	Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly	
82		90	95	100	
84	ggc	ctg	ccg	tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc	544
85	Gly	Leu	Pro	Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro	
86	105	110	115	120	
88	gtc	gtc	gcg	atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg	592
89	Val	Val	Ala	Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala	
90		125	130	135	
92	gtg	cct	ggc	agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat	640
93	Val	Pro	Gly	Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp	
94		140	145	150	
96	tcg	ctg	acc	ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat	688
97	Ser	Leu	Thr	Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp	
98		155	160	165	
100	gcc	gcg	atc	cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta	736
101	Ala	Ala	Ile	Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu	
102		170	175	180	
104	gga	cag	gtg	gtc ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg	784
105	Gly	Gln	Val	Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu	
106	185	190	195	200	
108	tcc	cag	ggt	ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg	832
109	Ser	Gln	Gly	Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala	
110		205	210	215	
112	atc	gcg	ggc	cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc	880
113	Ile	Ala	Gly	Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile	
114		220	225	230	
116	ggg	cct	acc	gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac	928
117	Gly	Pro	Thr	Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	
118		235	240	245	
120	ggc	gca	cga	gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc	976
121	Gly	Ala	Arg	Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu	
122		250	255	260	
124	ggc	atc	tcc	acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc	1024
125	Gly	Ile	Ser	Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile	
126	265	270	275	280	

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130          285          290          295
132 gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca 1120
133 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
134          300          305          310
136 ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga tttcgtcgcg 1166
137 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
138          315          320
140 gataccaccc gccggccggc caattggatt ggccgccagcc gtgattgccg cgtgagcccc 1226
142 cgagttccgt ctcccgctgcg cgtggcatcg tggaagcaat gaacgaggca gaacacagcg 1286
144 tcgagcacc cccgtgacg ggcagtcacg tcgaaggcgg tgtggtcgag catccggatg 1346
146 ccaaggactt cgcagcgcc gccgccctgc ccgccgatcc gacctggttt aagcacgcgc 1406
148 tcttctacga ggtgctggtc cggcgcttct tcgacgccag cgcggacggt tccggcgatc 1466
150 tgcgtggact catcgatcgc ctcgactacc tgcagtggct tggcatcgac tgcattctggt 1526
152 tgccgccggt ctacgactcg ccgctgcgcg acggcggtta cgacattcgc gacttctaca 1586
154 aggtgctgcc cgaattcggc accgtcgacg atttcgtcgc cctggtcgac gccgctcacc 1646
156 ggcgaggat cgcgcatcat accgacctgg tgatgaatca cacctcggag tcgcacccct 1706
158 ggtttcagga gtccgcgcgc gaccagacg gaccgtacgg tgactattac gtgtggagcg 1766
160 acaccagcga gcgctacacc gacgcccgga tcattctcgt cgacaccgaa gagtcgaact 1826
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166 <211> LENGTH: 355
167 <212> TYPE: PRT
168 <213> ORGANISM: Mycobacterium tuberculosis
170 <220> FEATURE:
171 <223> OTHER INFORMATION: 32 KD serine protease MTB32A
173 <400> SEQUENCE: 2
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175 1 5 10 15
176 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
177 20 25 30
178 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
179 35 40 45
180 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
181 50 55 60
182 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
183 65 70 75 80
184 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
185 85 90 95
186 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
187 100 105 110
188 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
189 115 120 125
190 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
191 130 135 140
192 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
193 145 150 155 160
194 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu

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195          165          170          175
196 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
197          180          185          190
198 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
199          195          200          205
200 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
201          210          215          220
202 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
203 225          230          235          240
204 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
205          245          250          255
206 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
207          260          265          270
208 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
209          275          280          285
210 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
211          290          295          300
212 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
213 305          310          315          320
214 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln
215          325          330          335
216 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
217          340          345          350
218 Pro Pro Ala
219          355
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 396
224 <212> TYPE: DNA
225 <213> ORGANISM: Mycobacterium tuberculosis
227 <220> FEATURE:
228 <223> OTHER INFORMATION: 14 KD C-terminal fragment of MTB32A Ra12
230 <220> FEATURE:
231 <221> NAME/KEY: CDS
232 <222> LOCATION: (1)..(396)
233 <223> OTHER INFORMATION: Ra12
235 <400> SEQUENCE: 3
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238 1 5 10 15
240 gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg 96
241 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
242 20 25 30
244 ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc 144
245 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
246 35 40 45
248 ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg 192
249 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
250 50 55 60
252 gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg 240

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TIME: 11:24:16

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04162002\I684215A.raw

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253 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
254 65 70 75 80
256 atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg 288
257 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
258 85 90 95
260 gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg 336
261 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
262 100 105 110
264 caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag 384
265 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
266 115 120 125
268 gga ccc ccg gcc 396
269 Gly Pro Pro Ala
270 130
273 <210> SEQ ID NO: 4
274 <211> LENGTH: 132
275 <212> TYPE: PRT
276 <213> ORGANISM: Mycobacterium tuberculosis
278 <220> FEATURE:
279 <223> OTHER INFORMATION: 14 KD C-terminal fragment of MTB32A Ra12
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285 20 25 30
286 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
287 35 40 45
288 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
289 50 55 60
290 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
291 65 70 75 80
292 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
293 85 90 95
294 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
295 100 105 110
296 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
297 115 120 125
298 Gly Pro Pro Ala
299 130
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303 <211> LENGTH: 702
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <221> NAME/KEY: CDS
309 <222> LOCATION: (4)..(696)
310 <223> OTHER INFORMATION: Ra12-DPPD fusion polypeptide
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Description of Artificial Sequence:Ra12-DPPD fusion

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VERIFICATION SUMMARY

DATE: 04/16/2002

PATENT APPLICATION: US/09/684,215A

TIME: 11:24:17

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04162002\I684215A.raw